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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of the claims in the application.

1. -2. (*Canceled*)

3. (*Currently amended*) A method in a computer system for ~~displaying data on~~ generating a graphic display for visualization of gene expression in a molecular topography, comprising:

providing a first set of data, the data comprising gene expression measurements and descriptive information for a first plurality of polynucleotides;

defining an X-Y plane having a first axis corresponding to sequence identifiers and a second axis corresponding to polynucleotide sizes;

(a) ~~generating a first gene expression profile within the X-Y plane for the first of a plurality of gene expression indicating polynucleotides including for each of the polynucleotides, the first profile comprising a plurality of peaks with each peak corresponding to a polynucleotide, the peak defined by:~~

(i) ~~a first value for a first polynucleotide characteristic comprising a sequence identifier for the polynucleotide;~~

(ii) ~~a second value for a second polynucleotide characteristic different from said first characteristic comprising a measure of size of the polynucleotide, wherein an intersection between the first value and the second value defines a point within the X-Y plane; and~~

(iii) at the point, plotting along a Z-axis intersecting the X-Y plane a third value that is a measure of the quantity of the polynucleotide;

~~(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and~~

~~(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby wherein the plurality of~~

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peaks is generated for the first plurality of polynucleotides so that the graphic display comprises a molecular topography of gene expression.

4.-24. (*Canceled*)

25. (*New*) The method of claim 3, further comprising:
providing a second set of data comprising gene expression measurements and descriptive information for a second plurality of polynucleotides;
generating a second gene expression profile within the X-Y plane for the second plurality of polynucleotides;
comparing the first and second gene expression profiles to generate a differential gene expression profile;
wherein the graphic display comprises the molecular topography of differential gene expression.

26. (*New*) The method of claim 25, wherein one of the first and second sets of data corresponds to a reference sample and the other of the first and second sets of data corresponds to a test sample.

27. (*New*) The method of claim 26, wherein the differential gene expression is diagnostic of a condition or disease.

28. (*New*) The method of claim 3, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first set of data in a temporal succession; and
generating and displaying gene expression profiles for each subsequent set of data to observe dynamic changes in gene expression over time.

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29. (New) The method of claim 28, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

30. (New) The method of claim 28, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.

31. (New) The method of claim 25, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first and second sets of data in a temporal succession; and
generating and displaying differential gene expression profiles for each subsequent set of data to observe dynamic changes in differential gene expression over time.

32. (New) The method of claim 31, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

33. (New) The method of claim 31, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.

34. (New) A method in a computer system for generating a graphic display for visualization of gene expression data, comprising:
providing a first set of data, the data comprising gene expression measurements and descriptive information for a first plurality of polynucleotides;
defining an X-Y plane having a first axis corresponding to sequence identifiers and a second axis corresponding to polynucleotide sizes;
plotting within the X-Y plane a plurality of points corresponding to the first plurality of polynucleotides according to their sequence identifiers and polynucleotide sizes; and
for each point within the plane, plotting along a Z-axis intersecting the X-Y plane a measured value corresponding to a quantity of mRNA produced for the polynucleotide plotted at the point so that a peak extending from the X-Y plane is generated;

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wherein the graphic display comprises a three-dimensional plot representative of gene expression for the first plurality of polynucleotides.

35. (*New*) The method of claim 34, further comprising:
providing a second set of data comprising gene expression measurements and descriptive information for a second plurality of polynucleotides;
generating a second gene expression profile within the X-Y plane for the second plurality of polynucleotides;
comparing the first and second gene expression profiles to generate a differential gene expression profile;
wherein the graphic display comprises the molecular topography of differential gene expression.

36. (*New*) The method of claim 35, wherein one of the first and second sets of data corresponds to a reference sample and the other of the first and second sets of data corresponds to a test sample.

37. (*New*) The method of claim 36, wherein the differential gene expression is diagnostic of a condition or disease.

38. (*New*) The method of claim 32, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first set of data in a temporal succession; and
generating and displaying gene expression profiles for each subsequent set of data to observe dynamic changes in gene expression over time.

39. (*New*) The method of claim 38, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

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40. (*New*) The method of claim 38, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process.

41. (*New*) The method of claim 35, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first and second sets of data in a temporal succession; and
generating and displaying differential gene expression profiles for each subsequent set of data to observe dynamic changes in differential gene expression over time.

42. (*New*) The method of claim 41, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

43. (*New*) The method of claim 41, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.